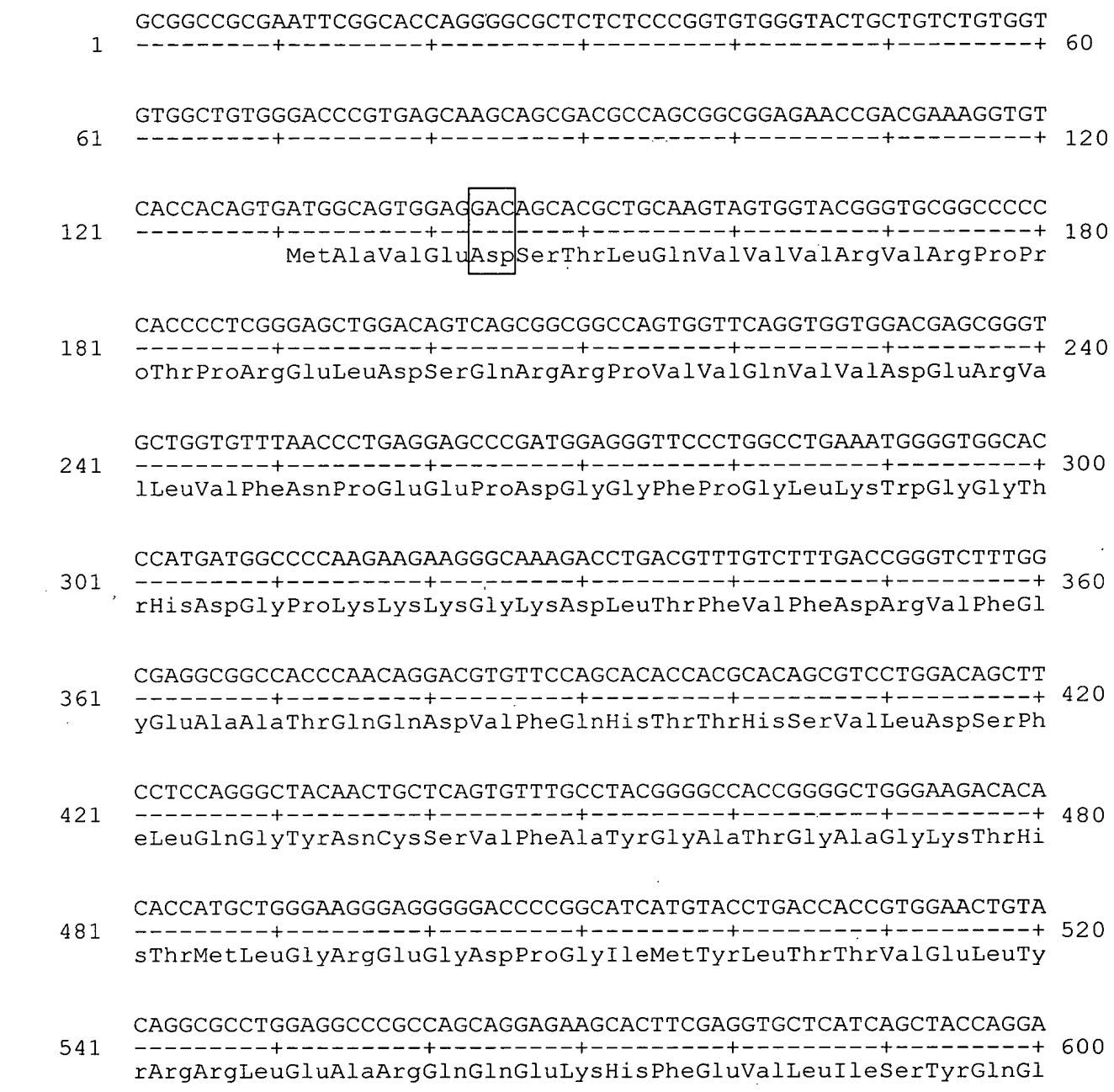

GCGGCCGCGAATTCGGCACCAGGGGCGCTCTCTCCCGGTGTGGGTACTGCTGTCTGTGGT
1 60
GTGGCTGTGGGACCCGTGAGCAAGCAGCGACGCCAGCGGCGGAGAACCGACGAAAGGTGT
61 120
CACCACAGTGATGGCAGTGGAGGACAGCACGCTGCAAGTAGTGGTACGGGTGCGGCCCCC
121 180
MetAlaValGluAspSerThrLeuGlnValValValArgValArgProPr
CACCCCTCGGGAGCTGGACAGTCAGCGGCGGCCAGTGGTTCAGGTGGTGGACGAGCGGGT
181 240
oThrProArgGluLeuAspSerGlnArgArgProValValGlnValValAspGluArgVa
GCTGGTGTTTAACCCTGAGGAGCCCGATGGAGGGTTCCCTGGCCTGAAATGGGGTGGCAC
241 300
lLeuValPheAsnProGluGluProAspGlyGlyPheProGlyLeuLysTrpGlyGlyTh
CCATGATGGCCCCAAGAAGAAGGGCAAAGACCTGACGTTTGTCTTTGACCGGGTCTTTGG
301 360
rHisAspGlyProLysLysLysGlyLysAspLeuThrPheValPheAspArgValPheGl
CGAGGCGGCCACCCAACAGGACGTGTTCCAGCACACCACGCACAGCGTCCTGGACAGCTT
361 420
yGluAlaAlaThrGlnGlnAspValPheGlnHisThrThrHisSerValLeuAspSerPh
CCTCCAGGGCTACAACTGCTCAGTGTTTGCCTACGGGGCCACCGGGGCTGGGAAGACACA
421 480
eLeuGlnGlyTyrAsnCysSerValPheAlaTyrGlyAlaThrGlyAlaGlyLysThrHi
CACCATGCTGGGAAGGGAGGGGGACCCCGGCATCATGTACCTGACCACCGTGGAACTGTA
481 520
sThrMetLeuGlyArgGluGlyAspProGlyIleMetTyrLeuThrThrValGluLeuTy
CAGGCGCCTGGAGGCCCGCCAGCAGGAGAAGCACTTCGAGGTGCTCATCAGCTACCAGGA
541 600
rArgArgLeuGluAlaArgGlnGlnGluLysHisPheGluValLeuIleSerTyrGlnGl

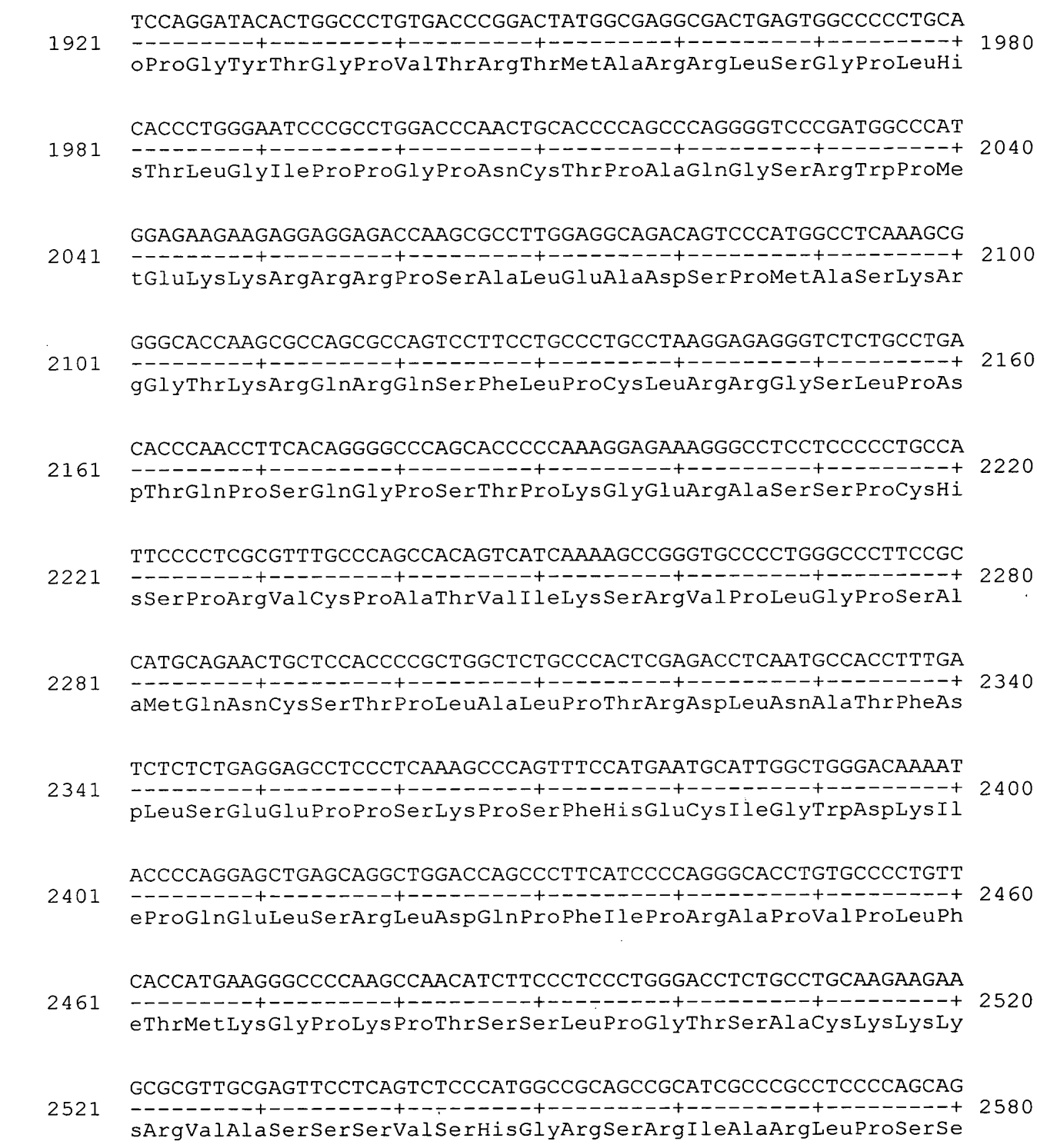
FIG. 1A


GGTGTATAATGAACAGATCCATGACCTCCTGGAGCCCAAGGGGCCCCTTGCCATCCGCGA
601 660
uValTyrAsnGluGlnIleHisAspLeuLeuGluProLysGlyProLeuAlaIleArgGl
GGACCCCGACAAGGGGGTGGTGGTGCAAGGACTTTCTTTCCACCAGCCAGCCTCAGCCGA
661 720
uAspProAspLysGlyValValValGlnGlyLeuSerPheHisGlnProAlaSerAlaGl
GCAGCTGCTGGAGATACTGACCAGGGGGAACCGTAACCGCACGCAGCACCCCACTGATGC
721 780
uGlnLeuLeuGluIleLeuThrArgGlyAsnArgAsnArgThrGlnHisProThrAspAl
CAACGCGACTTCCTCCCGCTCCCATGCCATCTTCCAGATCTTTGTGAAGCAGCAGGACCG
781 840
aAsnAlaThrSerSerArgSerHisAlaIlePheGlnIlePheValLysGlnGlnAspAr
GGTTCCAGGACTGACCCAGGCTGTCCAGGTGGCCAAGATGAGCCTGATTGACCTGGCTGG
841 900
gValProGlyLeuThrGlnAlaValGlnValAlaLysMetSerLeuIleAspLeuAlaGl
CTCAGAGCGGGCATCCAGCACCCATGCGAAGGGGGAGCGGCTGCGGGAGGGGGCCAACAT
901 960
ySerGluArgAlaSerSerThrHisAlaLysGlyGluArgLeuArgGluGlyAlaAsnIl
CAACCGCTCTCTGCTGGCGCTCATCAACGTCCTCAATGCCTTGGCCGATGCAAAGGGCCG
961 1020
eAsnArgSerLeuLeuAlaLeuIleAsnValLeuAsnAlaLeuAlaAspAlaLysGlyAr
CAAGACCCATGTGCCCTACCGGGACAGCAAACTGACCCGCCTGCTCAAAGACTCCCTCGG
1021 1080
gLysThrHisValProTyrArgAspSerLysLeuThrArgLeuLeuLysAspSerLeuGl
GGGCAACTGCCGCACAGTGATGATCGCTGCCATCAGCCCCTCCAGCCTGACCTACGAGGA
1081 1120
yGlyAsnCysArgThrValMetIleAlaAlaIleSerProSerSerLeuThrTyrGluAs
CACGTACAACACCCTCAAATATGCCGACCGGGCCAAGGAGATCAGGCTCTCGCTGAAGAG
1141 1200
pThrTyrAsnThrLeuLysTyrAlaAspArgAlaLysGluIleArgLeuSerLeuLysSe
CAATGTGACCAGCCTGGACTGTCACATCAGCCAGTATGCTACCATCTGCCAACAGCTCCA
1201 1260
rAsnValThrSerLeuAspCysHisIleSerGlnTyrAlaThrIleCysGlnGlnLeuGl

FIG. 1B

```
                GGCTGAGGTAGCCGCTCTGAGGAAGAAGCTCCAAGTGTATGAGGGGGGAGGCCAGCCCCC
1261  ---------+---------+---------+---------+---------+---------+---------+ 1320
                nAlaGluValAlaAlaLeuArgLysLysLeuGlnValTyrGluGlyGlyGlyGlnProPr

                ACCACAGGACCTCCCAGGATCTCCCAAGTCGGGACCACCACCAGAACACCTTCCCAGCTC
1321  ---------+---------+---------+---------+---------+---------+---------+ 1380
                oProGlnAspLeuProGlySerProLysSerGlyProProProGluHisLeuProSerSe

                CCCCTTGCCACCCCACCCTCCCAGCCAGCCCTGCACCCCAGAGCTCCCTGCAGGGCCTAG
1381  ---------+---------+---------+---------+---------+---------+---------+ 1440
                rProLeuProProHisProProSerGlnProCysThrProGluLeuProAlaGlyProAr

                AGCCCTTCAAGAGGAGAGTCTGGGGATGGAGGCCCAGGTGGAGAGGGCCATGGAAGGGAA
1441  ---------+---------+---------+---------+---------+---------+---------+ 1500
                gAlaLeuGlnGluGluSerLeuGlyMetGluAlaGlnValGluArgAlaMetGluGlyAs

                CTCTTCAGACCAGGAGCAGTCCCCAGAGGATGAGGATGAAGGCCCAGCTGAGGAGGTTCC
1501  ---------+---------+---------+---------+---------+---------+---------+ 1560
                nSerSerAspGlnGluGlnSerProGluAspGluAspGluGlyProAlaGluGluValPr

                AACCCAGATGCCAGAGCAGAACCCCACACATGCACTGCCAGAGTCCCCTCGCCTGACCCT
1561  ---------+---------+---------+---------+---------+---------+---------+ 1620
                oThrGlnMetProGluGlnAsnProThrHisAlaLeuProGluSerProArgLeuThrLe

                GCAGCCCAAGCCAGTCGTGGGCCACTTCTCAGCACGGGAACTGGATGGGGACCGTTCTAA
1621  ---------+---------+---------+---------+---------+---------+---------+ 1680
                uGlnProLysProValValGlyHisPheSerAlaArgGluLeuAspGlyAspArgSerLy

                GCAGTTGGCCCTAAAGGTGCTGTGCGTTGCCCAGCGGCAGTACTCCCTGCTCCAAGCAGC
1681  ---------+---------+---------+---------+---------+---------+---------+ 1740
                sGlnLeuAlaLeuLysValLeuCysValAlaGlnArgGlnTyrSerLeuLeuGlnAlaAl

                CAACCTCCTGACGCCCGACATGATCACAGAGTTTGAGACCCTACAGCAGCTGGTGCAAGA
1741  ---------+---------+---------+---------+---------+---------+---------+ 1800
                aAsnLeuLeuThrProAspMetIleThrGluPheGluThrLeuGlnGlnLeuValGlnGl

                GGAAAAAATTGAGCCTGGGGCAGAGGCCTTGAGGACTTCAGGCCTGGCCAGGGGGGCACC
1801  ---------+---------+---------+---------+---------+---------+---------+ 1860
                uGluLysIleGluProGlyAlaGluAlaLeuArgThrSerGlyLeuAlaArgGlyAlaPr

                TCTGGCTCAGGAGCTGTGTTCAGAGTCAATCCCTGTGCCGTCTCCTCTCTGCCCAGAGCC
1861  ---------+---------+---------+---------+---------+---------+---------+ 1920
                oLeuAlaGlnGluLeuCysSerGluSerIleProValProSerProLeuCysProGluPr
```

FIG. 1C


TCCAGGATACACTGGCCCTGTGACCCGGACTATGGCGAGGCGACTGAGTGGCCCCCTGCA
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oProGlyTyrThrGlyProValThrArgThrMetAlaArgArgLeuSerGlyProLeuHi
1980
CACCCTGGGAATCCCGCCTGGACCCAACTGCACCCCAGCCCAGGGGTCCCGATGGCCCAT
1981
sThrLeuGlyIleProProGlyProAsnCysThrProAlaGlnGlySerArgTrpProMe
2040
GGAGAAGAAGAGGAGGAGACCAAGCGCCTTGGAGGCAGACAGTCCCATGGCCTCAAAGCG
2041
tGluLysLysArgArgArgProSerAlaLeuGluAlaAspSerProMetAlaSerLysAr
2100
GGGCACCAAGCGCCAGCGCCAGTCCTTCCTGCCCTGCCTAAGGAGAGGGTCTCTGCCTGA
2101
gGlyThrLysArgGlnArgGlnSerPheLeuProCysLeuArgArgGlySerLeuProAs
2160
CACCCAACCTTCACAGGGGCCCAGCACCCCCAAAGGAGAAAGGGCCTCCTCCCCCTGCCA
2161
pThrGlnProSerGlnGlyProSerThrProLysGlyGluArgAlaSerSerProCysHi
2220
TTCCCCTCGCGTTTGCCCAGCCACAGTCATCAAAAGCCGGGTGCCCCTGGGCCCTTCCGC
2221
sSerProArgValCysProAlaThrValIleLysSerArgValProLeuGlyProSerAl
2280
CATGCAGAACTGCTCCACCCCGCTGGCTCTGCCCACTCGAGACCTCAATGCCACCTTTGA
2281
aMetGlnAsnCysSerThrProLeuAlaLeuProThrArgAspLeuAsnAlaThrPheAs
2340
TCTCTCTGAGGAGCCTCCCTCAAAGCCCAGTTTCCATGAATGCATTGGCTGGGACAAAAT
2341
pLeuSerGluGluProProSerLysProSerPheHisGluCysIleGlyTrpAspLysIl
2400
ACCCCAGGAGCTGAGCAGGCTGGACCAGCCCTTCATCCCCAGGGCACCTGTGCCCCTGTT
2401
eProGlnGluLeuSerArgLeuAspGlnProPheIleProArgAlaProValProLeuPh
2460
CACCATGAAGGGCCCCAAGCCAACATCTTCCCTCCCTGGGACCTCTGCCTGCAAGAAGAA
2461
eThrMetLysGlyProLysProThrSerSerLeuProGlyThrSerAlaCysLysLysLy
2520
GCGCGTTGCGAGTTCCTCAGTCTCCCATGGCCGCAGCCGCATCGCCCGCCTCCCCAGCAG
2521
sArgValAlaSerSerSerValSerHisGlyArgSerArgIleAlaArgLeuProSerSe
2580

FIG. 1D

```
                CACTTTGAAGAGGCCAGCTGGGCCCCTTGTACTCCCAGAGCTGCCCTTGAGTCCCCTGTG
2581  ---------+---------+---------+---------+---------+---------+---------+ 2640
                rThrLeuLysArgProAlaGlyProLeuValLeuProGluLeuProLeuSerProLeuCy

                CCCTAGCAACCGGAGGAATGGAAAGGACCTCATCAGGGTGGGGAGAGCGCTCTCAGCAGG
2641  ---------+---------+---------+---------+---------+---------+---------+ 2700
                sProSerAsnArgArgAsnGlyLysAspLeuIleArgValGlyArgAlaLeuSerAlaGl

                GAACGGCGTCACCAAGGTGTCCTGACCGCCAGAATGTCCTGACCACCAAGGTGTCCTAAC
2701  ---------+---------+---------+---------+---------+---------+---------+ 2760
                yAsnGlyValThrLysValSer

                CTACCGGCCCCTCTGCTGGATACCCCTCTTGGACCTGTAGCCACCTGCACCAGGAGCTGG
2761  ---------+---------+---------+---------+---------+---------+---------+ 2820

                ACCTGCCTTCCTTACCTGGGAGCAATTAGTGCCAACACACCTTTGCTGTATTAACATCCC
2821  ---------+---------+---------+---------+---------+---------+---------+ 2880

                TCCCCAGACATCCATCCTGCTACTCACCCTCTGTTAATCTCCTGTTACACTCAGCTTCTT
2881  ---------+---------+---------+---------+---------+---------+---------+ 2940

                GGCATGTACATATTCATTTGTGAGTGTTAATGTGCTGCTGTTTTTTGTTTTTTGGTGGTT
2941  ---------+---------+---------+---------+---------+---------+---------+ 3000

                TTTGTTTTTTGTTTTTTTTGTTTTGAGATGGAGTCTTACTCTGTCGCCCAGGCTGGAGTG
3001  ---------+---------+---------+---------+---------+---------+---------+ 3060

                CAGTGGTACGATCTTGGCTCACTGCAACCTCCGCCTCCTGGGTTCAAGTAATTCTCCTGC
3061  ---------+---------+---------+---------+---------+---------+---------+ 3120

                CTCAGCTTTCCAAGTAGCTGGGATTACAGGCACCCATCACCACACCCAGCTAATTTTCGT
3121  ---------+---------+---------+---------+---------+---------+---------+ 3180

                CTTTTTAATAGAGAGGGGGTTTTTCCATGTTGGCCAGGCTGGTCTTGAACTCCTGACCTC
3181  ---------+---------+---------+---------+---------+---------+---------+ 3240

                AGGTGATCCGCCTGCCTCAGCTTCCCAAAGTGCTGAGATTACAGGCATGAGCTACCACGC
3241  ---------+---------+---------+---------+---------+---------+---------+ 3300

                CTGGCCCGTGTTGCTGTTTTAAAGGTGCTGCCATGTTCCCCCATCTTTTTTTTTTTTGAG
3301  ---------+---------+---------+---------+---------+---------+---------+ 3360
```

FIG. 1E

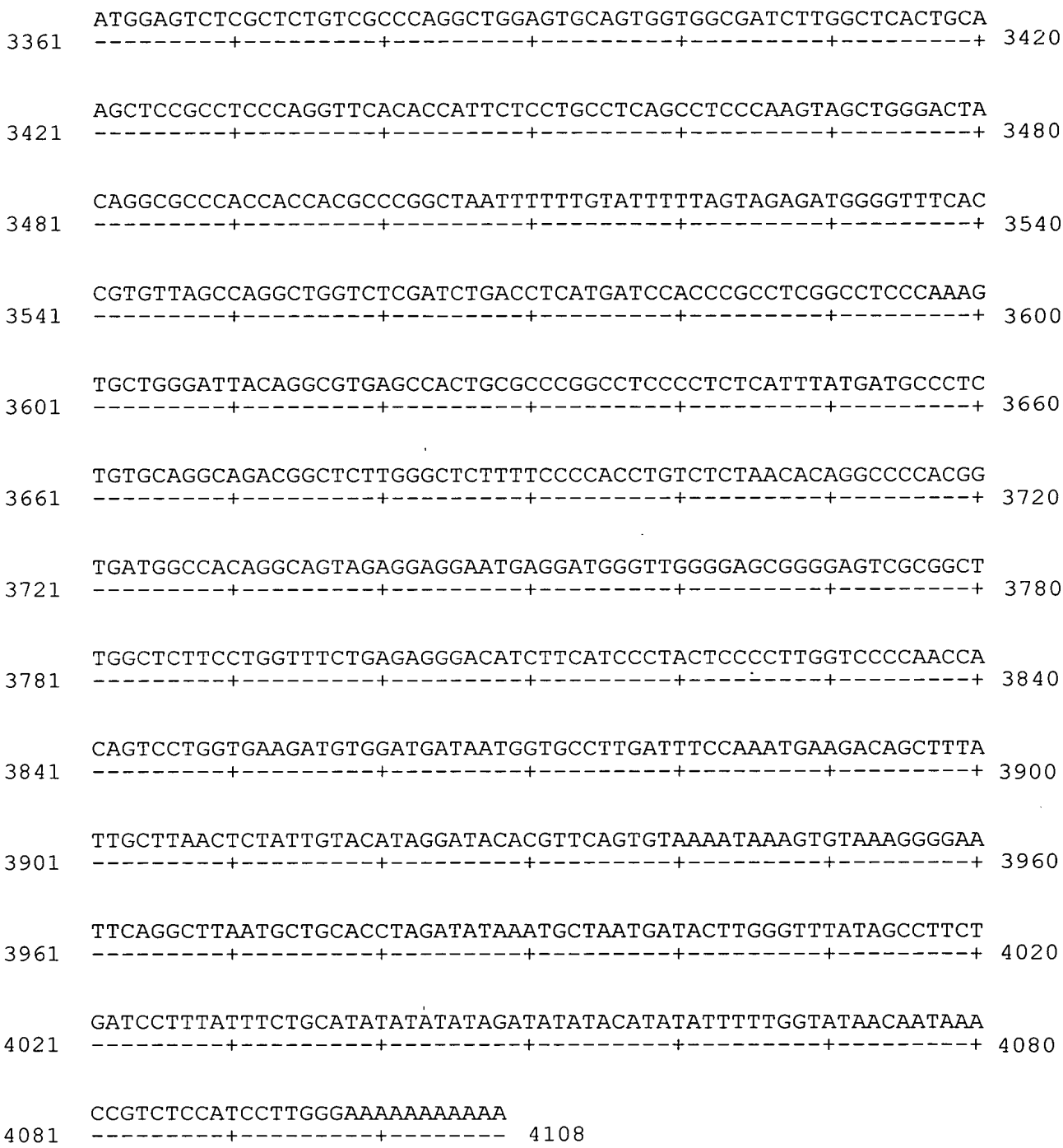

ATGGAGTCTCGCTCTGTCGCCCAGGCTGGAGTGCAGTGGTGGCGATCTTGGCTCACTGCA
3361 ---------+---------+---------+---------+---------+---------+ 3420
AGCTCCGCCTCCCAGGTTCACACCATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTA
3421 ---------+---------+---------+---------+---------+---------+ 3480
CAGGCGCCCACCACCACGCCCGGCTAATTTTTTGTATTTTTAGTAGAGATGGGGTTTCAC
3481 ---------+---------+---------+---------+---------+---------+ 3540
CGTGTTAGCCAGGCTGGTCTCGATCTGACCTCATGATCCACCCGCCTCGGCCTCCCAAAG
3541 ---------+---------+---------+---------+---------+---------+ 3600
TGCTGGGATTACAGGCGTGAGCCACTGCGCCCGGCCTCCCCTCTCATTTATGATGCCCTC
3601 ---------+---------+---------+---------+---------+---------+ 3660
TGTGCAGGCAGACGGCTCTTGGGCTCTTTTCCCCACCTGTCTCTAACACAGGCCCCACGG
3661 ---------+---------+---------+---------+---------+---------+ 3720
TGATGGCCACAGGCAGTAGAGGAGGAATGAGGATGGGTTGGGGAGCGGGGAGTCGCGGCT
3721 ---------+---------+---------+---------+---------+---------+ 3780
TGGCTCTTCCTGGTTTCTGAGAGGGACATCTTCATCCCTACTCCCCTTGGTCCCCAACCA
3781 ---------+---------+---------+---------+---------+---------+ 3840
CAGTCCTGGTGAAGATGTGGATGATAATGGTGCCTTGATTTCCAAATGAAGACAGCTTTA
3841 ---------+---------+---------+---------+---------+---------+ 3900
TTGCTTAACTCTATTGTACATAGGATACACGTTCAGTGTAAAATAAAGTGTAAAGGGGAA
3901 ---------+---------+---------+---------+---------+---------+ 3960
TTCAGGCTTAATGCTGCACCTAGATATAAATGCTAATGATACTTGGGTTTATAGCCTTCT
3961 ---------+---------+---------+---------+---------+---------+ 4020
GATCCTTTATTTCTGCATATATATATAGATATATACATATATTTTTGGTATAACAATAAA
4021 ---------+---------+---------+---------+---------+---------+ 4080
CCGTCTCCATCCTTGGGAAAAAAAAAAA
4081 ---------+---------+-------- 4108

FIG. 1F

```
  1  GACAGCACGC TGCAAGTAGT GGTACGGGTG CGGCCCCCCA CCCCTCGGGA GCTGGACAGT
 61  CAGCGGCGGC CAGTGGTTCA GGTGGTGGAC GAGCGGGTGC TGGTGTTTAA CCCTGAGGAG
121  CCCGATGGAG GGTTCCCTGG CCTGAAATGG GGTGGCACCC ATGATGGCCC CAAGAAGAAG
181  GGCAAAGACC TGACGTTTGT CTTTGACCGG GTCTTTGGCG AGGCGGCCAC CCAACAGGAC
241  GTGTTCCAGC ACACCACGCA CAGCGTCCTG GACAGCTTCC TCCAGGGCTA CAACTGCTCA
301  GTGTTTGCCT ACGGGGCCAC CGGGGCTGGG AAGACACACA CCATGCTGGG AAGGGAGGGG
361  GACCCCGGCA TCATGTACCT GACCACCGTG GAACTGTACA GGCGCCTGGA GGCCCGCCAG
421  CAGGAGAAGC ACTTCGAGGT GCTCATCAGC TACCAGGAGG TGTATAATGA ACAGATCCAT
481  GACCTCCTGG AGCCCAAGGG GCCCCTTGCC ATCCGCGAGG ACCCCGACAA GGGGGTGGTG
541  GTGCAAGGAC TTTCTTTCCA CCAGCCAGCC TCAGCCGAGC AGCTGCTGGA GATACTGACC
601  AGGGGGAACC GTAACCGCAC GCAGCACCCC ACTGATGCCA ACGCGACTTC CTCCCGCTCC
661  CATGCCATCT TCCAGATCTT TGTGAAGCAG CAGGACCGGG TTCCAGGACT GACCCAGGCT
721  GTCCAGGTGG CCAAGATGAG CCTGATTGAC CTGGCTGGCT CAGAGCGGGC ATCCAGCACC
781  CATGCGAAGG GGGAGCGGCT GCGGGAGGGG GCCAACATCA ACCGCTCTCT GCTGGCGCTC
841  ATCAACGTCC TCAATGCCTT GGCCGATGCA AAGGGCCGCA AGACCCATGT GCCCTACCGG
901  GACAGCAAAC TGACCCGCCT GCTCAAAGAC TCCCTCGGGG GCAACTGCCG CACAGTGATG
961  ATCGCTGCCA TCAGCCCCTC CAGCCTGACC TACGAGGACA CGTACAACAC CCTC
```

FIG. 2

```
  1  DSTLQVVVRV RPPTPRELDS QRRPVVQVVD ERVLVFNPEE PDGGFPGLKW GGTHDGPKKK
 61  GKDLTFVFDR VFGEAATQQD VFQHTTHSVL DSFLQGYNCS VFAYGATGAG KTHTMLGREG
121  DPGIMYLTTV ELYRRLEARQ QEKHFEVLIS YQEVYNEQIH DLLEPKGPLA IREDPDKGVV
181  VQGLSFHQPA SAEQLLEILT RGNRNRTQHP TDANATSSRS HAIFQIFVKQ QDRVPGLTQA
241  VQVAKMSLID LAGSERASST HAKGERLREG ANINRSLLAL INVLNALADA KGRKTHVPYR
301  DSKLTRLLKD SLGGNCRTVM IAAISPSSLT YEDTYNTL
```

FIG. 3

MAVEDSTLQVVVRVRPPTPRELDSQRRPVVQVVDERVLVFNPEEPDGGFPGLKWGGT
HDGPKKKGKDLTFVFDRVFGEAATQQDVFQHTTHSVLDSFLQGYNCSVFAYGATGAG
KTHTMLGREGDPGIMYLTTVELYRRLEARQQEKHFEVLISYQEVYNEQIHDLLEPKG
PLAIREDPDKGVVVQGLSFHQPASAEQLLEILTRGNRNRTQHPTDANATSSRSHAIF
QIFVKQQDRVPGLTQAVQVAKMSLIDLAGSERASSTHAKGERLREGANINRSLLALI
NVLNALADAKGRKTHVPYRDSKLTRLLKDSLGGNCRTVMIAAISPSSLTYEDTYNTL
KYADRAKEIRLKGNSKLEGKPIPNPLLGLDSTRTGHHHHHH

FIG. 4

ATGGCAGTGGAGGACAGCACGCTGCAAGTAGTGGTACGGGTGCGGCCCCCCACCCCT
CGGGAGCTGGACAGTCAGCGGCGGCCAGTGGTTCAGGTGGTGGACGAGCGGGTGCTG
GTGTTTAACCCTGAGGAGCCCGATGGAGGGTTCCCTGGCCTGAAATGGGGTGGCACC
CATGATGGCCCCAAGAAGAAGGGCAAAGACCTGACGTTTGTCTTTGACCGGGTCTTT
GGCGAGGCGGCCACCCAACAGGACGTGTTCCAGCACACCACGCACAGCGTCCTGGAC
AGCTTCCTCCAGGGCTACAACTGCTCAGTGTTTGCCTACGGGGCCACCGGGGCTGGG
AAGACACACACCATGCTGGGAAGGGAGGGGGACCCCGGCATCATGTACCTGACCACC
GTGGAACTGTACAGGCGCCTGGAGGCCCGCCAGCAGGAGAAGCACTTCGAGGTGCTC
ATCAGCTACCAGGAGGTGTATAATGAACAGATCCATGACCTCCTGGAGCCCAAGGGG
CCCCTTGCCATCCGCGAGGACCCCGACAAGGGGGTGGTGGTGCAAGGACTTTCTTTC
CACCAGCCAGCCTCAGCCGAGCAGCTGCTGGAGATACTGACCAGGGGGAACCGTAAC
CGCACGCAGCACCCCACTGATGCCAACGCGACTTCCTCCCGCTCCCATGCCATCTTC
CAGATCTTTGTGAAGCAGCAGGACCGGGTTCCAGGACTGACCCAGGCTGTCCAGGTG
GCCAAGATGAGCCTGATTGACCTGGCTGGCTCAGAGCGGGCATCCAGCACCCATGCG
AAGGGGGAGCGGCTGCGGGAGGGGGCCAACATCAACCGCTCTCTGCTGGCGCTCATC
AACGTCCTCAATGCCTTGGCCGATGCAAAGGGCCGCAAGACCCATGTGCCCTACCGG
GACAGCAAACTGACCCGCCTGCTCAAAGACTCCCTCGGGGGCAACTGCCGCACAGTG
ATGATCGCTGCCATCAGCCCCTCCAGCCTGACCTACGAGGACACGTACAACACCCTC
AAATATGCCGACCGGGCCAAGGAGATCAGGCTCAAGGGCAATTCGAAGCTTGAAGGT
AAGCCTATCCCTAACCCTCTCCTCGGTCTCGATTCTACGCGTACCGGTCATCATCAC
CATCACCATTGA

FIG. 5

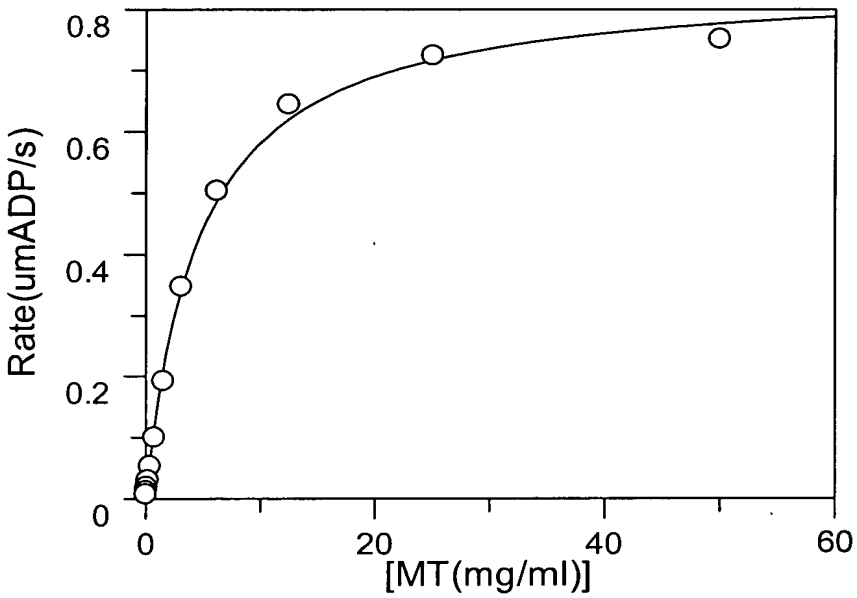
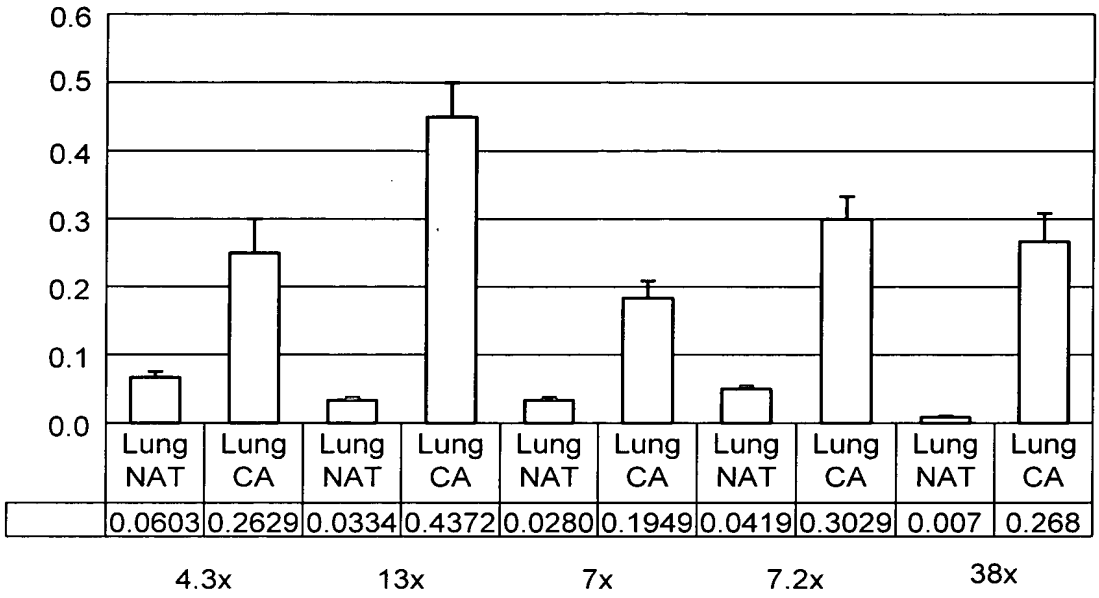


FIG. 6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0.5
0.4
0.3
0.2
0.1
0.0
Lung NAT
Lung CA
Lung NAT
Lung CA
Lung NAT
Lung CA
Lung NAT
Lung CA
Lung NAT
Lung CA
0.0603
0.2629
0.0334
0.4372
0.0280
0.1949
0.0419
0.3029
0.007
0.268
4.3x
13x
7x
7.2x
38x

FIG. 7A

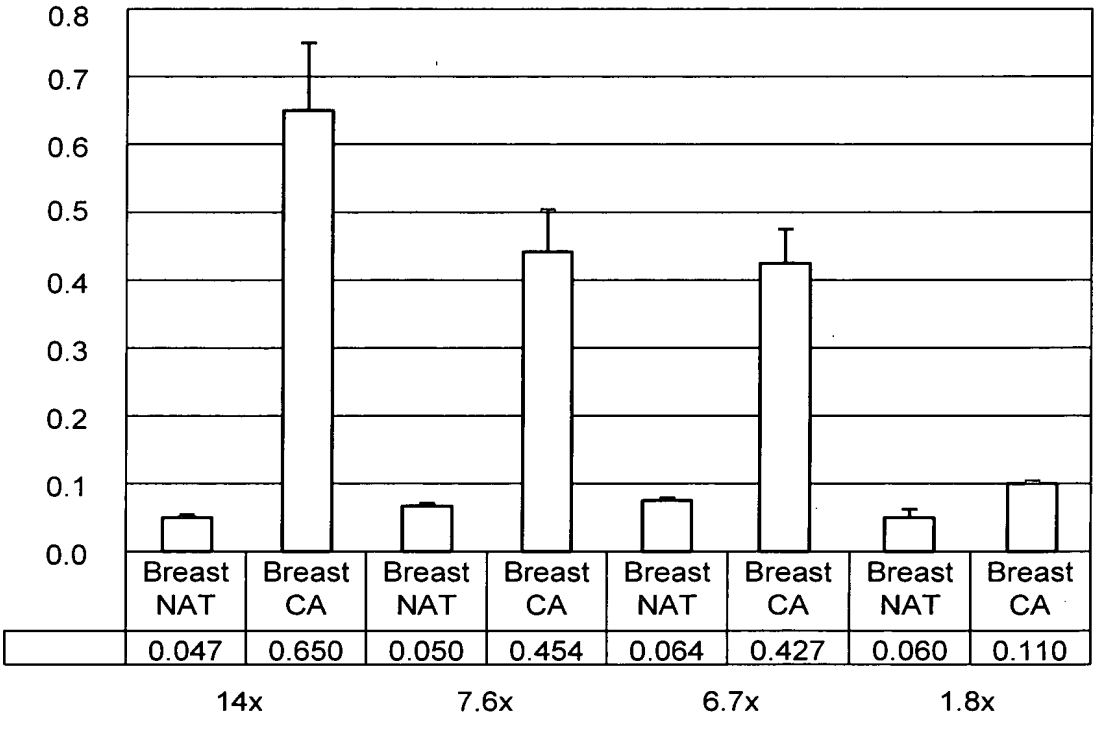
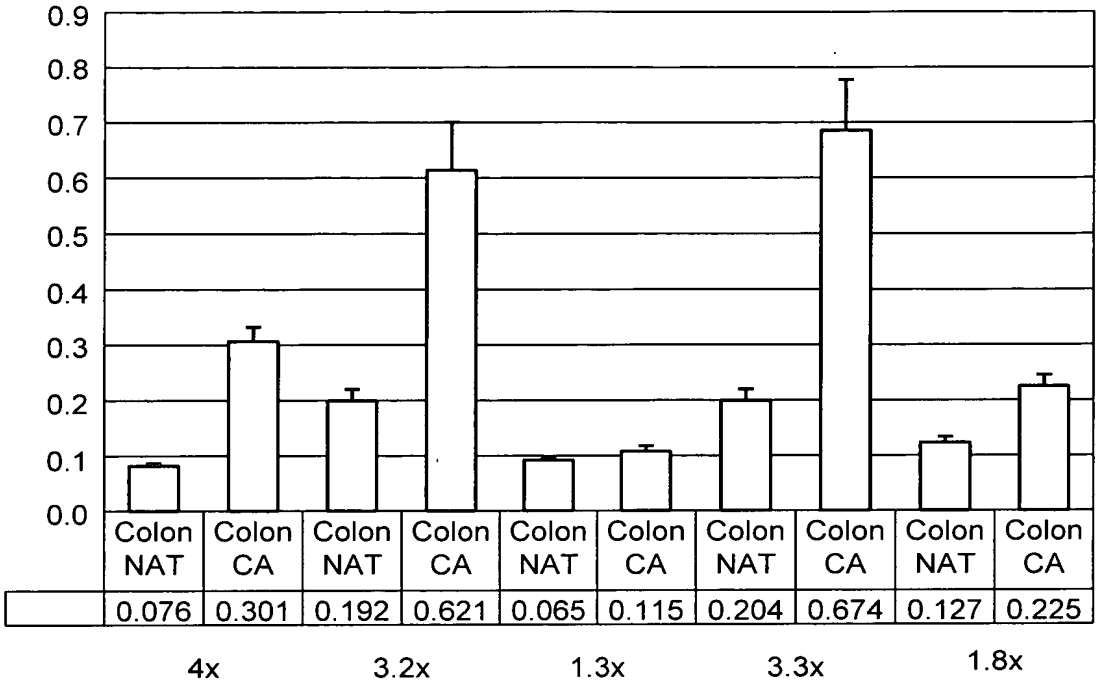

0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
Breast NAT
Breast CA
Breast NAT
Breast CA
Breast NAT
Breast CA
Breast NAT
Breast CA
0.047
0.650
0.050
0.454
0.064
0.427
0.060
0.110
14x
7.6x
6.7x
1.8x

FIG. 7B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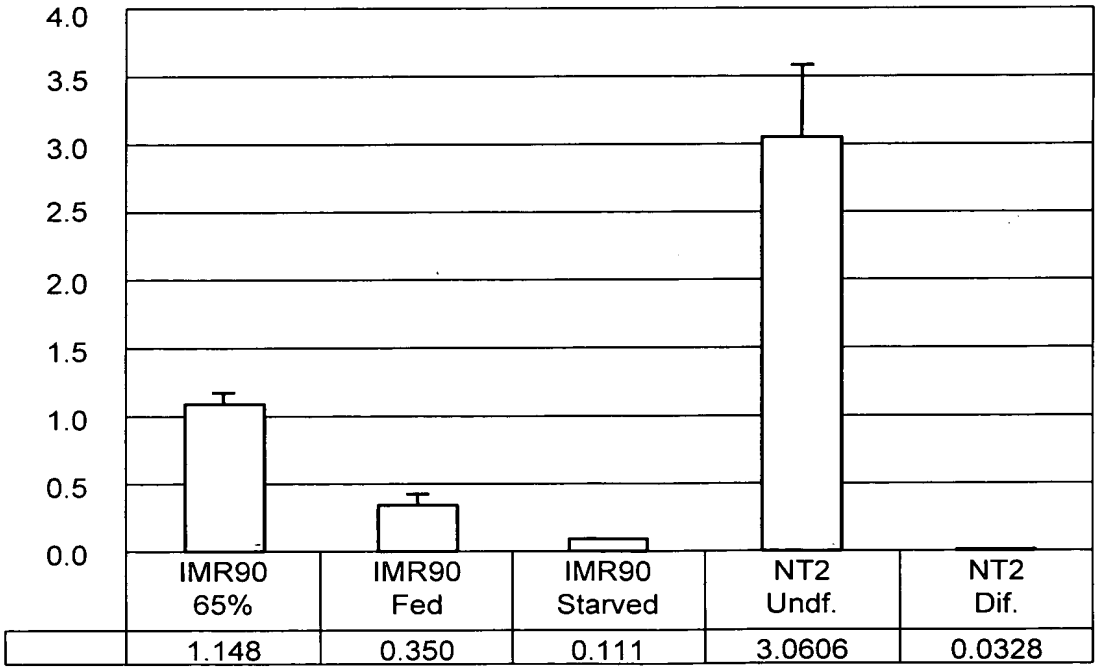
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
Colon NAT
Colon CA
Colon NAT
Colon CA
Colon NAT
Colon CA
Colon NAT
Colon CA
Colon NAT
Colon CA
0.076
0.301
0.192
0.621
0.065
0.115
0.204
0.674
0.127
0.225
4x
3.2x
1.3x
3.3x
1.8x

FIG. 7C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3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
IMR90 65%
IMR90 Fed
IMR90 Starved
NT2 Undf.
NT2 Dif.
1.148
0.350
0.111
3.0606
0.0328

FIG. 7D